GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

OM protein - protein search, using sw model

Run

March 1, 2001, 16:10:44; Search time 32.86 Seconds (without alignments) 113.650 Million cell upo

cell updates/sec

Perfect score: US-09-331-631A-25_COPY_31_85 315 1 ENPKHNKCLQSCNSERDSYR.....

Sequence: ENPKHNKCLQSCNSERDSYR......EECEEGEIPRPRPRPQHPER 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database 1: 2: 3: PIR_66:* pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	Į.	14	13	12	11	10	9	8	7	6	ហ	4	ω	2	1		Result
58	58	58	58	58	8	58.5	5	59	59	59	59	59.5	60	60	61	61	62	62	62	N)	62.5	63	ω.	63.5	5	9.	w	315		Score
18.4	18.4	18.4	18.4	18.4	18.6		18.7	18.7	18.7	•	18.7		19.0	19.0	-	19.4	19.7	19.7	19.7	•	19.8	•	0	20.2	0		100.0	100.0		Query
799	799	798	478	81	1610	411	1390	713	344	281	199	174	2203	1646	1952	147	462	390	389	3051	588	663	414	373	774	639	605	605		I.enath
N	-	N	N	N	N	N	2	N	N	N	N	N	2	N	N	ω	2	2	N	N	μ	N	N	N	N	N	N	H	: 6	⊒ #
JC4126	IJMSFB	S01659	T03750	A45320	A46227	I51285	36	A35502	S34153	D29960	T28981	BQICIT	T42742	JH0422	T48814	T26225	T00708	S44285	149640	S42373	FWCNAB	T26835	T21954	T21955	T39539	B24810	S20007	FWSYBA		-
integrin beta olig	fibronectin recept	integrin beta-1 ch	violaxanthin de-ep	transglutaminase s	voltage-dependent			пr	prote	Balbiani ring 6 ch	hypothetical prote	Balbiani ring-1 ch	voltage-dependent	3			ф	1	3		٠.	_			alpha-amylase homo			beta-conglycinin a	pescription	

45	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30
57	57	57	57	57	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	58	58	58
18.1	18.1	18.1	18.1	18.1	18.3	18.3	18.3	18.3	18.3	18.3	18.3	18.3	18.4	18.4	18.4
633	572	511	403	223	1300	566	542	422	337	231	179	131	2181	2161	803
2	Ν	N	2	Ν	N	N	ب	N	2	Ν	N	Н	N	N	-
T47524	T29880	S24345	S02709	S43535	A36502	S22477	A54963	T51199	T27635	T14801	S28256	BGBO2	A38198	JH0564	Г ЈСН3
hypothetical prote	hypothetical prote	Balbiani ring 1 pr	ear-2 protein - hu	evel protein - zeb	insulin receptor-r	vicilin precursor	transcription fact	hypothetical prote	homeobox protein c	MADS box protein M	NADH dehydrogenase	spermatid transiti	calcium channel al	calcium channel al	integrin, band 3 p

ALIGNMENTS

RESULT FWSYBA

beta-conglycinin alpha chain precursor - soybean (Species: Glycine max (soybean) (C;Species: Glycine max (soybean) (C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999 (C;Accession: S14681; S74124; S06714 (R;Sebastiani, F.L.; Farrell, L.B.; Schuler, M.A.; Beachy, R.N. Plant Mol. Biol. 15, 197-201, 1990 (A;Title: Complete sequence of a cDNA of alpha subunit of soybean beta-conglycinin. A;Reference number: S14681; MUID:91355860 (R;Sebastion: S14681)

A; Molecule type: mRNA A; Residues: 1.605 <SEB>

A;Cross-references: EMBL:X17698; NID:g18535; PIDN:CAA35691.1; PID:g18536 R;Shutov, A.D.; Kakhovskaya, I.A.; Bastrygina, A.S.; Bulmaga, V.P.; Horstmann, Eur. J. Blochem. 241, 221-228, 1996

A; Title: Limited proteolysis of beta-conglycinin and glycinin, A; Reference number: S74123; MUID:97054613

the 7S and 11S storage

C.; Mu

A;Accession: S74124
A;Molecule type: protein
A;Residues: 189-196,'H',198,'N',200,'X',202-203;397-408,'X',410,'X',412-417,'X',419-4
A;Experimental source: seed

C; Superfamily: glycinin

C:Keywords: glycoprotein; seed; storage protein F;1-22/Domain: signal sequence #status predicted <SIG> F;23-62/Domain: propeptide #status predicted <PRO> F:63-605/Product: beta-conglycinin alpha chain #status predicted <MAT> F:261,517/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match
Best Local Similarity
Matches 55; Conserv 100.0%; Score 315; DB 1; 100.0%; Pred. No. 1.1e-26; vative 0; Mismatches 0; Length 605;

1 ENPKHNKCLQSCNSERDSYRNQACHARCNLLKVEKEECEEGEIPRPRPRPQHPER 55

Conservative

Indels

0;

Gaps

0;

31 ENPKHNKCLQSCNSERDSYRNQACHARCNLLKVEKEECEEGEIPRPRPRPRPQHPER 85

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S20007

beta-conglycinin alpha chain precursor - soybean C;Species: Glycine max (soybean) C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997 C;Accession: S20007 R;Lelievre, J.M.; Dickinson, C.D.; Dickinson, L.A.; Nielsen, N.C. Plant Mol. Biol. 18, 259-274, 1992

A;Title: Synthesis and assembly of soybean beta-conglycinin in vitro A;Reference number: S20007; MUID:92119248
A;Accession: S20007

A; Status: preliminary

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alpha-amylase homolog - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
C;Accession: T39539
R;Wood, V:; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
submitted to the EMBL Data Library, February 1998
A;Reference number: 221862
A;Accession: T39539
A;Accession: T39539
A;Accession: T39539
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-774 <WOOD
A;Cross-references: EMBL:AL021748; PIDN:CAA16864.1; GSPDB:GN00067; SPDB:SPBC16A3.13
A;Experimental Source: strain 972h-; cosmid c16A3
C;Genetics:
A;Gene: SPDB:SPBC16A3.13
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M13759; NID:g169928; PIDN:AAB01374.1; PID:g169929
A;Note: the authors translated the codon GGT for residue 352 as Glu
R;Schuler, M.A.; Schmitt, E.S.; Beachy, R.N.
Nucleic Acids Res. 10, 8225-8244, 1982
A;Title: Closely related families of genes code for the alpha and alpha'
A;Reference number: S16337; MUID:83143288
A;Accession: S16337; MUID:83143288
A;Accession: S16337 MUID:83143288
C;Genetics: 361-639 <SCH>
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C:Species: Glycine max (soybean)
C:Date: 07-Mar-1988 #sequence_revision 30-Jun-1991 #text_change 20-Aug-1999
C:Accession: B24810; S16337
R:Doyle, J.J.; Schuler, M.A.; Godette, W.D.; Zenger, V.; Beachy, R.N.; Slightom, J.L.
J. Biol. Chem. 261, 9228-9238, 1986
A;Title: The glycosylated seed storage proteins of Glycine max and Phaseolus vulgaris.
A;Reference number: A24810; MUID:86250867
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-639 <DNA
A;R
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C; Superfamily: glycinin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QNPSHNKCLRSCNSEKDSYRNQACHARCNLLKVEEEEECEEGQI--PRPRPQHPER 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278/1; 355/3; 382/3; 481/3; 575/1
          16;
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          Conservative
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Pred. No. 1.2e-20;
5; Mismatches 1
                                       Score
Pred.
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Pred. No. 1.1e-26;
core 65.5; D
red. No. 12;
Mismatches
                                                                           DB
                                                                       2;
       20;
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R; Lennard, N. submitted to the EMBL Data Library, June A: Reference number: Z19493
                                    hypothetical protein Y43F4A.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F38B7.1a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A;Molecule type: DNA
A;Residues: 1-373 <WILL>
A;Cross-references: EMBL:274033; PIDN:CAA98476.1; GSPDB:GN00023; CESP:F38B7.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F38B7.1b - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #te
C; Accession: R; Matthews, 1
                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:F38B7.la
A;Map position: 5
A;Introns: 30/2; 53/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: T21954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, A; Reference number: Z19493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 5
A; Introns: 12/3; 81/2; 116/1; 221/2; 317/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: clone F38B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession:
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Best Local Similarity 35.7
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 HKCKEHCSCHHDKFPRPVPH----NGTKPDHKPWKHEEHCHHGKFPRPVPHNGTKPDH
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20; Conserv
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                                                                                                                                                                                                                                                                   Score 63.5; Di
Pred. No. 12;
7; Mismatches
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Pred. No. 11;
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                                                                                                                                                                                                                                                                                                          Length 414;
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C;Keywords: glycoprotein; seeu; string relicted <SIG>F;1-25/Domain: signal sequence #status predicted <F;26-588/Product: alpha-globulin storage proprotein #status predicted F;417/Binding site: carbohydrate (Asn) (covalent) #status predicted
hypothetical protein T20G5.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 07-Oct-1994 #sequence revision 10-Nov-1005 #+-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: not compared with conceptual translation A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-81 <CH2> C;Comment: This is a seed storage protein. C;Superfamily: glycinin C;Keywords: glycoprotein; seed; storage protein C;Keywords: glycoprotein; seed; storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PIE A;Experimental source: var. Coker 201 R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant MOI. Biol. 9, 533-546, 1987 A;Title: Developmental biochemistry of cottonseed embryogenesis A;Reference number: S06398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-globulin B precursor (clone C72) - upland cotton RyAlternate names: seed storage protein; vicilin precursor C:Species: Gossypium hirsutum (upland cotton) C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999 C:Accession: A30838; S06911 R:Cchan, C.A.: Pyle, J.B.: Legocki, A.B.: Dure III, L. Plant Mol. Biol. 7, 475-489, 1986 A:Title: Developmental biochemistry of cottonseed embryogenesis and germinal A:Title: Developmental B:Title: Developm
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S42373
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A; Introns: 29/3; 120/2; 159/3; 187/2; 273/2; 310/3; 360/3; 393/2;
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A; Residues: 1-588 < CHL>
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A; Accession: A30838
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                            EDPQRRYEECQQECRQQEERQRPQ-CQQRC-LKRFEQEQQQSQRQFQECQQ----HCHQQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KCLQSCNSERDSYRNQACHARCNLLKVEKEECEEGEIPR 45
                                                                                                                                                                                                                                                                                      EQRPER 140
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Pred. No. 20;
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Pred. No. 20;
4; Mismatches
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    10-Nov-1995 #text_change 16-Jul-1999
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Gene 142, 313-314, 1994
A;Title: The sequence of a murine cDNA encoding Ear-2, A;Reference number: 149640; MUID:94252389
                                                                                     R:Jonk, L.J.; de Jonge, M.E.; Pals, C.E.; Wissink, S.; Vervaart, J.M.; Schoorlemmer, Mech. Dev. 47, 81-97, 1994
A:Title: Cloning and expression during development of three murine members of the COU A:Reference number: 148305; MUID:95034311
A:Accession: 148734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: ear-2
C;Superfamily: unassigned erbA-related proteins; erbA transforming
C;Keywords: zinc finger
                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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A; Residues: 1-389 < RE:
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C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Sep-1999
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    A; Cross-references:
                      A; Molecule type: mRNA
A; Residues: 1-390 < RES>
                                                               A; Status: preliminary; translated
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A;Cross-references: GB:L25674; NID:g409757; PIDN:AAA37532.1;
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A; Residues: 1-3051 <SMI>
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                                                                                                                                                                                                                                                                                                                                                                        TCRSNRDCQIDQHHRNQCQYCRLKKCFRVGMRKEAVQRGRIPHALPGP 139
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16; Conserv
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EMBL: X76654; NID: g482929;
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25.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 62; DB Pred. No. 16; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62.5;
Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                March 1994
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                                                                 GB/EMBL/DDBJ
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16;
  PIDN:CAA54097.1;
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  PID:g482930
                                                                                                                                                                                                                      20-Sep-1999
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hypothetical protein W06D11.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T26225
R:Lloyd, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eologis, A.; Ecker, J.R.
submitted to the EMBL Data Library,
submitted for Genomic sequence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: unassigned erbA-related C;Keywords: zinc finger F;55-300/Domain: erbA transforming prot
                                                                                                                                                                                                  A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                                                                                       A; Residues: 1-147 <WIL>
                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: T26225
                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, A; Reference number: Z20176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-462 <SHI>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: Z14200
A; Accession: T00708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, eologis, A.; Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           violaxanthin de-epoxidase homolog F22013.3 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: ATSP: F22013.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: translated from GB/EMBL/DDBJ
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                                                                       Query Match
Best Local Similarity
                                                                                                                                               Map position:
Introns: 103/3
                                                                                                                                                                                  Gene: CESP:W06D11.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 CLQTCNNRPD----ETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDP 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 TCRSNRDCQIDQHHRNQCQYCRLKKCFRVGMRKEAVQRGRIPHALPGP 139
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mes 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 CLQSCNSERDSYRNQACHARC------NLLKVEKEEC-----EEGEIPRPRP 48
Similarity 33. 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T00708
                                                       Conservative
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erbA transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                 EMBL: z69718; PIDN: CAA93537.1; GSPDB: GN00028; CESP: W06D11.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL:AC003981; NID:g3063438; PID:g3063441; GSPDB:GN00059; ATSP:F220:
se: cultivar Columbia
                                                                                                                                                                                                                    clone W06D11
                                                                       19.4%;
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27.6%;
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33.3%;
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                                                                       Score 61;
Pred. No.
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Pred. No.
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Arabidopsis thaliana
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                                                                                        Length 147;
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                  48
                                                       Indels
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            A; Experimental source: kidney C; Comment: Calcium channels a:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position:
A; Introns: 281/:
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                                                                                                                                                                                                                                                                                     A; Accession: D35901
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: JH0422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neuron 7, 35-44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Hui, A.; Ellinor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: NCSP:15E6.220
A;Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T48814
R;Schulte, U.; Aign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: 224541
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Best Local :
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24.7%;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1040-1261,1305-1365 <RES>
                                                                                                                                                             A; Reference number: A46422; MUID:93066265
A; Accession: I60901
                                                                                                                                                                                                                    R;Yu, A.S.L.; Hebert, S.C.; Brenner, B.M.; Lytton, Proc. Natl. Acad. Sci. U.S.A. 89, 10494-10498, 1992
A;Tille: Molecular characterization and nephron dis
                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; A;Molecule type: mRNA A;Residues: 1247-1434 <SNU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Snutch, T.P.; Leonard, J.P.; Gilbert, M.M.; Lester, H.A.; Proc. Natl. Acad. Sci. U.S.A. 87, 3391-3395, 1990 A;Tille: Rat brain expresses a heterogeneous family of calci A;Reference number: A35901; MUID:90239020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-1646 <HUI>
A;Residues: 1-1646 <HUI>
A;Cross-references: GB:M57682; NID:g206573; PIDN:AAA42015.1; PID:g206574
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; MOLECULE TYPE:
A; Residues: 1-1952 <SCH>
A; Residues: 1-1952 <SCH>
A; Cross-references: EMBL: AL353822; GSPDB: GN00112;
A: Fynarimental source: cosmid contig 15E6; strain
                                                   A;Cross-references: GB:M99221; NID:g203370; PIDN:AAA40895.1; PID:g203371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Molecular cloning of multiple subtypes of a novel rat brain isoform of the \lambda; Reference number: JH0422; MUID:91299338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Jan-2000
C;Accession: JH0422; D35901; I60901
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C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      voltage-dependent calcium channel complex alpha-1 chain - rat
C; Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              585 SPEDNEVPMSVDPDRDDSQSELSEPPDEDILLPDAPDHVMETVEKEEAEEDDDDEARSQS 644
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Calcium channels are essential for many cellular functions, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aign, V.; Hoheisel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.T.; Krizanova, O.; Wang, J.J.; Diebold, R.J.; Schwartz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Database,
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85;
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April 2000
                                                                                                                                                                                                                          distribution
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74
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muscle
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C:Superfamily: voltage-depindent calcium channel protein alpha-1 chain C:Keywords: alternative glicing; calcium binding; calcium channel; glycoprotein; phosph F:1463-1491/Domain: calcium binding #status predicted <EFC>
F:154,224,328/Binding s/te: carbohydrate (Asn) (covalent) #status predicted F:464,848,1489,1584/Binding site: phosphate (Ser) (covalent) #status predicted
```

Qy Query Match 19.0%; Score 60; DB 2; Length 1646; Best Local Similarity 34.9%; Pred. No. 94; Matches 22; Conservative 9; Mismatches 18; Indels 14; Gaps

4.

47 RPR 49

Search completed: March 1, 2001, 16:10:46 Job time: 1077 sec

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843 RPR 845

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